

Amendments to the Specification

Please replace the last paragraph on page 3, continuing onto page 4, with the following amended paragraph:

Figure 6A-D depicts a multiple sequence alignment (MSA) of the amino acid sequences encoded by fourteen known or predicted microbial *coaX* genes. ~~SEQ ID NOs: 2-15~~ correspond to the amino acid sequences of: *Bacillus subtilis* (SwissProt™ Accession No. P37564; SEQ ID NO:2), *Clostridium acetobutylicum* (WIT™ Accession No. RCA03301, Argonne National Laboratories; SEQ ID NO:3), *Streptomyces coelicolor* (PIR™ Accession No. T36391; SEQ ID NO:4), *Mycobacterium tuberculosis* (SwissProt™ Accession No. O06282; SEQ ID NO:5), *Rhodobacter capsulatus* (WIT™ Accession No. RRC02473; SEQ ID NO:6), *Desulfovibrio vulgaris* (DBJ™ Accession No. BAA21476.1; SEQ ID NO:59), *Deinococcus radiodurans* (SwissProt™ Accession No. Q9RX54; SEQ ID NO:8), *Thermotoga maritima* (GenBank™ Accession No. AAD35964.1; SEQ ID NO:9), *Treponema pallidum* (SwissProt™ Accession No. O83446; SEQ ID NO:10), *Borrelia burgdorferi* (SwissProt™ Accession No. O51477; SEQ ID NO:11), *Aquifex aeolicus* (SwissProt™ Accession No. O67753; SEQ ID NO:12), *Synechocystis sp.* (SwissProt™ Accession No. P74045; SEQ ID NO:13), *Helicobacter pylori* (SwissProt™ Accession No. O25533; SEQ ID NOs: 14 or 67), and *Bordetella pertussis* (SwissProt™ Accession No. Q45338; SEQ ID NO:15). ~~respectively.~~ The alignment was generated using ClustalW MSA software at the GenomeNet CLUSTALW Server at the Institute for Chemical Research, Kyoto University. The following parameters were used: Pairwise Alignment, K-tuple (word) size = 1, Window size = 5, Gap Penalty = 3, Number of Top Diagonals = 5, Scoring Method = Percent; Multiple Alignment, Gap Open Penalty = 10, Gap Extension Penalty = 0.0, Weight Transition = No, Hydrophilic residues = Gly, Pro, Ser, Asn, Asp, Gln, Glu, Arg and Lys, Hydrophobic Gaps = Yes; and Scoring Matrix = BLOSUM.